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Figure 1



Figure 2

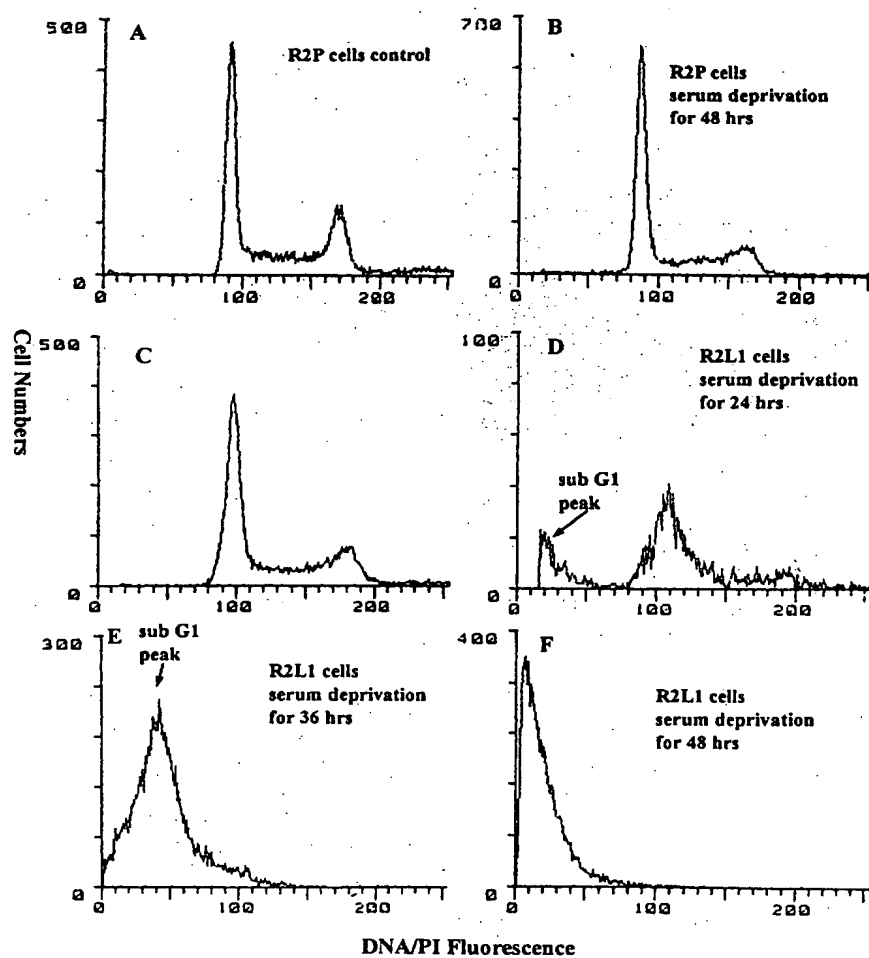


Figure 3

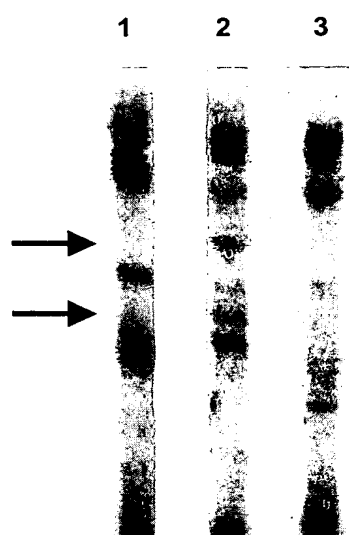


Figure 4

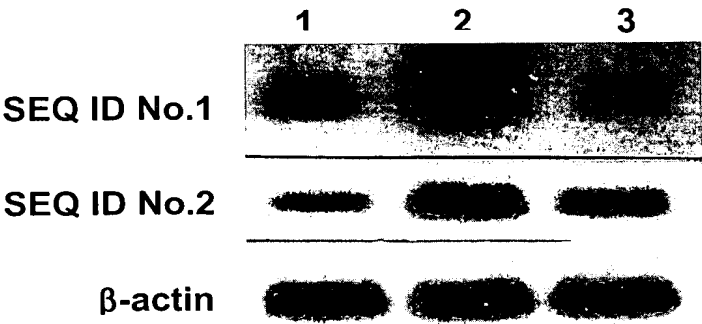


Figure 5

**DNA Sequence of ARBP cDNA (SEQ ID No. 3) and predicted amino acid
sequence of encoded protein (SEQ ID No. 4)**

```
GCTGGCCGGGTCGACCCTGGTGTTCATCCGTTTAGGAAGCGGCTTCACCGCCAACAGCACGGCC
1  Met Ala Gly Ala Leu Val Arg Lys Ala Ala Asp Tyr Val Arg Ser Lys Asp Phe Arg Asp
   ATG GCT GGA GCT CTG GTG CGC AAA GCA GCG GAC TAT GTC CGG AGC AAG GAC TTC CGG GAC
21  Tyr Leu Met Ser Thr His Phe Trp Gly Pro Val Ala Asn Trp Gly Leu Pro Ile Ala Ala
   TAT CTC ATG AGT ACG CAC TTC TGG GGC CCA GTT GCC AAC TGG GGT CTC CCC ATT GCT GCT
41  Ile Asn Asp Met Lys Lys Ser Pro Glu Ile Ile Ser Gly Arg Met Thr Phe Ala Leu Cys

   ATC AAT GAC ATG AAG AAA TCT CCA GAG ATT ATC AGT GGG CGG ATG ACT TTC GCC CTC TGT
61  Cys Tyr Ser Leu Thr Phe Met Arg Phe Ala Tyr Lys Val Gln Pro Arg Asn Trp Leu Leu
   TGC TAT TCT CTG ACA TTC ATG AGA TTT GCC TAC AAG GTA CAA CCC CGA AAC TGG CTT CTG
81  Phe Ala Cys His Val Thr Asn Glu Val Ala Gln Leu Ile Gln Gly Gly Arg Leu Ile Asn
   TTT GCG TGC CAT GTG ACA AAC GAA GTC GCT CAG CTC ATT CAG GGA GGA CGA CTT ATC AAC
101 Tyr Glu Met Ser Lys Arg Pro Ser Ala  *
    TAC GAG ATG AGT AAG CGG CCA TCT GCC TAG
CAGTGCAAGGACCAGCTCTTGAAAGGGACAGTGCT
CCAGCCACTGTTGCGGCCACAGATCACGTCAGCATGAATAGTCGTGCTGAGGGGAAAACACGGAAGACTATCTTTAATGACCATG
CCAACATTATTGAATAGCCAAGAATCCCCAAACCAACTCTCGGCTGCCTTATCAATGCTAAACTTTATTTGTCTTCATCAGGAGT
AGTTCAAAATATGCAGCTAATTTAATAATTTTGAATGATGTTATCTATAGCAATCTGTAGTAATATGTATATTATCTATTGGGAT
TTGTGTAATAAAAAATCTAAGGGAACAAAACCTTTATAACTACAAGCACTTAAGTCCTCAAAATTCTTGACTTTTTCTTTAATGAC
TATAGTATAACCCTCAGTTGGTCACATGTCTACACATAATTTCCAGTGATAACAAGTAGCGGTGTTTCCATATGTAATTCAGAT
CTGAACCTAATGGCAATAAATGGTTTAAATATTTGCGAAAAAAAAAAAA
```

Figure 6

Sequence 1: human 102 aa
Sequence 2: rat 109 aa
Sequence 3: mouse 109 aa

Sequences (1:2) Aligned. Score: 97.0588
Sequences (1:3) Aligned. Score: 96.0784
Sequences (2:2) Aligned. Score: 100
Sequences (2:3) Aligned. Score: 99.0826
Sequences (3:2) Aligned. Score: 99.0826
Sequences (3:3) Aligned. Score: 100

```
rat      MAGALVRKAADYVRSKDFRDYLMSTHFWGPVANWGLPIAAINDMKKSPEIISGRMTFALC
mouse    MAGALVRKAADYVRSKDFRDYLMSTHFWGPVANWGLPIAAINDMKKSPEIISGRMTFALC
human    MAGALVRKAADYVRSKDFRDYLMSTHFWGPVANWGLPIAAINDMKKSPEIISGRMTFALC
*****
```

```
rat      CYSLTFMRFAYKVQPRNWLLFACHVTNEVAQLIQGGRLINYEMSKRPSA
mouse    CYSQTFMRFAYKVQPRNWLLFACHVTNEVAQLIQGGRLINYEMSKRPSA
human    CYSLTFMRFAYKVQPRNWLLFACHATNEVAQLIQGGRLIKHE-----
*** *****.*****:.*
```

Figure 7

QUERY IS SEQ ID. No. 3, SUBJECT IS HUMAN

Homo sapiens NM_016098, mRNA
Length = 988

Score = 361 bits (182), Expect = 1e-96
Identities = 284/318 (89%)
Strand = Plus / Plus

```
Query: 56  gcacggccatggctggagctctggtgcgcaaagcagcggactatgtccggagcaaggact 115
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 115  gcacagccatggcgggcgcgttggtgcggaaaagcggcggactatgtccgaagcaaggatt 174

Query: 116  tccgggactatctcatgagtacgcacttctggggcccagttgccaaactggggtctcccca 175
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 175  tccgggactacctcatgagtacgcacttctggggcccagtagccaaactggggtcttccca 234

Query: 176  ttgctgctatcaatgacatgaagaaatctccagagattatcagtgggcggatgactttcg 235
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 235  ttgctgccatcaatgatgatgaaaaagtctccagagattatcagtgggcggatgacatttg 294

Query: 236  ccctctgttgctattctctgacattcatgagatttgccctacaagggtacaaccccgaaact 295
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 295  ccctctgttgctattctttgacattcatgagatttgccctacaagggtacagcctcggaact 354

Query: 296  ggcttctgtttgcgtgccatgtgacaaaagtcgctcagctcattcaggaggagcagac 355
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 355  ggcttctgtttgcatgccacgcaacaaatgaagtagcccagctcatccaggaggggcggc 414

Query: 356  ttatcaactacgagatga 373
          ||||| ||||| |||||
Sbjct: 415  ttatcaaacacgagatga 432
```

Score = 56.0 bits (28), Expect = 1e-04
Identities = 31/32 (96%)
Strand = Plus / Plus

```
Query: 857  aacttaatggcaataaatggtttaaatatttg 888
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 926  aacttaatggcaataaatgatttaaatatttg 957
```

Score = 46.1 bits (23), Expect = 0.092
Identities = 32/35 (91%)
Strand = Plus / Plus

```
Query: 595  gagtagttcaaaatatgcagctaattttaataattt 629
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 660  gagtagctcaaaatatgcaatttaattttaataattt 694
```

Score = 44.1 bits (22), Expect = 0.36
Identities = 95/118 (80%), Gaps = 1/118 (0%)
Strand = Plus / Plus

```
Query: 651  atctgtagtaatatgtatattatctattgggatttggtgaataaaaaatctaagggaaca 710
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 708  atctgcagtaatatgtatattatctattagaatttacttaataaaaaactgaagagaaca 767
```

```
Query: 711  aaactttataactacaagcacttaagtcctcaaaattcttgactttttctttaatgac 768
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 768  aaa-tttgtaaccactagcacttaagtactcctgattcttaacattgtctttaatgac 824
```


Figure 8

QUERY IS SEQ ID NO. 3, SUBJECT IS MOUSE

Mus musculus adult male kidney cDNA, RIKEN full-length enriched library,
clone:0610007A16 product:brain protein 44-like, full insert sequence
Length = 886
Score = 1374 bits (693), Expect = 0.0
Identities = 833/875 (95%), Gaps = 6/875 (0%)
Strand = Plus / Plus

Query: 19 ggtgtcatccgttttaggaagcggttcaccgccaacagcacggccatggctggagctctg 78
Sbjct: 13 ggtgtcatctgtctaggtagcggttcaccgccaacggcacggccatggctggagcgctg 72

Query: 79 gtgcgc aaagcagcggactatgtccggagcaaggacttccgggactatctcatgagtacg 138
Sbjct: 73 gtgcgc aaagcggcggactatgtccggagcaaggacttccgggactatctcatgagtacg 132

Query: 139 cacttctggggccagttgccaaactggggtctccccattgctgctatcaatgacatgaag 198
Sbjct: 133 cacttctggggccagttgccaaactggggtctccccattgctgctatcaatgacatgaag 192

Query: 199 aaatctccagagattatcagtgggcggatgactttcgccctctgttgctattctctgaca 258
Sbjct: 193 aaatctccagagattatcagtgggcggatgactttcgccctctgttgctattctctgaca 252

Query: 259 ttcattgagatttgcctacaagggtacaaccccgaaactgggtctgtttgctgcatgtg 318
Sbjct: 253 ttcattgagatttgcctacaagggtacaacctcgaaactgggtctgtttgctgcatgtg 312

Query: 319 acaaacgaagtcgctcagctcattcaggaggagcagacttatcaactacgagatgagtaag 378
Sbjct: 313 acaaacgaagtagctcagctcattcaggaggagcagacttatcaactacgagatgagtaag 372

Query: 379 cggccatctgcctagcagtgcaaggaccagctcttgaaagggacagtgctccagccactg 438
Sbjct: 373 cggccatctgcatagcgggtacaaggaccagctcttgaaagagacagtgctccagccactg 432

Query: 439 ttgcgccacagatcacgtcagcatgaatagtcgtgctgaggggaaaacacggaagacta 498
Sbjct: 433 ctgcagccacagatcatgtcagcatgagtagtcgtgctgaagggaaaacacagaatgcta 492

Query: 499 tctttaatgaccatgccaacattattgaatagccaagaatccccaaaccaactctcggt 558
Sbjct: 493 tc-ttaatgaccatgccaacattattgaatagccgagagtccttaaacccactctctgct 551

Query: 559 gccttatcaatgctaaactttatttgccttcacagagtagttcaaaatagcagctaa 618
Sbjct: 552 gccttatcaatgctaaaccttatttgccttcacagagtagttcaaaatagcaactaa 611

Query: 619 ttaataattttgaatgatg---ttatctatagcaatctgtagtaatatgtatattatct 675
Sbjct: 612 ttaataattttgaatgatggtttatctatagcaatctgtagtaatatgtatattatct 671

Query: 676 attgggattttgtgtaataaaaaatctaagggaacaaaactttataactacaagcactaa 735
Sbjct: 672 attgggattttgtgtaataaaaaatctaagggaacaaaactttataactacaagcactaa 731

Query: 736 gtccctcaaaattcttgactttttctttaatgactatagtataacccctcagttgggtcacat 795
Sbjct: 732 gtactcaaaattcttgactttttctttaatgacaatagta-aacccctcagttgggtcacat 790

Query: 796 gtctacacataatttccagtgataaacaagtagcggtgttttccatatgtaattcagatct 855
Sbjct: 791 gtctacacataatttccagtgataaacaagtagcggtgttttccatatgtaactcagatct 850

Query: 856 g-aacttaatggcaataaatgggtttaaatatttgc 889
Sbjct: 851 gtaacttaatggcaataaatgggtttaaatatttgc 885

Figure 9

SUBJECT IS MOUSE, QUERY IS HUMAN
Homo sapiens NM_016098, mRNA
Length = 988
Score = 404 bits (204), Expect = e-110
Identities = 291/320 (90%)
Strand = Plus / Plus

```
Query: 48  cggcacggccatggctggagcgctggtgcgcaaaagcggcggactatgtccggagcaagga 107
           |||||
Sbjct: 113  cggcacagccatggcgggcgcttgggtgcgaaagcggcggactatgtccgaagcaagga 172

Query: 108  cttccgggactatctcatgagtacgcacttctggggcccagttgccaaactggggtctccc 167
           |||||
Sbjct: 173  tttccgggactacctcatgagtacgcacttctggggcccagtagccaactggggtcttcc 232

Query: 168  cattgctgctatcaatgacatgaagaaatctccagagattatcagtggcgatgacttt 227
           |||||
Sbjct: 233  cattgctgcatcaatgatatgaaaaagtctccagagattatcagtggcgatgacatt 292

Query: 228  cgccctctgttgctattctctgacattcatgagatttgcctacaaggtacaacctcgaaa 287
           |||||
Sbjct: 293  tgccctctgttgctattctttgacattcatgagatttgcctacaaggtacagcctcgaa 352

Query: 288  ctggcttttgtttgcatgccatgtaacaaacgaagtagctcagctcattcagggaggacg 347
           |||||
Sbjct: 353  ctggcttctgtttgcatgccacgcaacaaatgaagtagcccagctcatccagggaggcg 412

Query: 348  acttatcaactacgagatga 367
           |||||
Sbjct: 413  gcttatcaaacacgagatga 432
```

Score = 63.9 bits (32), Expect = 4e-07
Identities = 35/36 (97%)
Strand = Plus / Plus

```
Query: 849  ctgtaacttaatggcaataaatgggtttaaataatttg 884
           |||||
Sbjct: 922  ctgtaacttaatggcaataaatgatttaaataatttg 957
```

Score = 58.0 bits (29), Expect = 2e-05
Identities = 35/37 (94%)
Strand = Plus / Plus

```
Query: 586  aagagtagttcaaaatatgcaactaatttaataattt 622
           |||||
Sbjct: 658  aagagtagctcaaaatatgcaattaatttaataattt 694
```

Score = 52.0 bits (26), Expect = 0.001
Identities = 96/118 (81%), Gaps = 1/118 (0%)
Strand = Plus / Plus

```
Query: 647  atctgtagtaatatgtatattatctattgggatttgtgtaataaaaaatctaagggaaca 706
           |||||
Sbjct: 708  atctgcagtaatatgtatattatctattagaatttacttaatgaaaaactgaagagaaca 767

Query: 707  aaattttataactacaagcacttaagtactcaaaattcttgactttttctttaatgac 764
           |||||
Sbjct: 768  aaa-tttgtaaccactagcacttaagtactcctgattcttaacattgtctttaatgac 824
```

Score = 46.1 bits (23), Expect = 0.091
Identities = 35/39 (89%)
Strand = Plus / Plus

```
Query: 519  aatagccgagagtccttaaacccactctctgctgcctta 557
           |||||
Sbjct: 589  aatagctgagagtttctaaaccaactctctgctgcctta 627
```

Figure 10

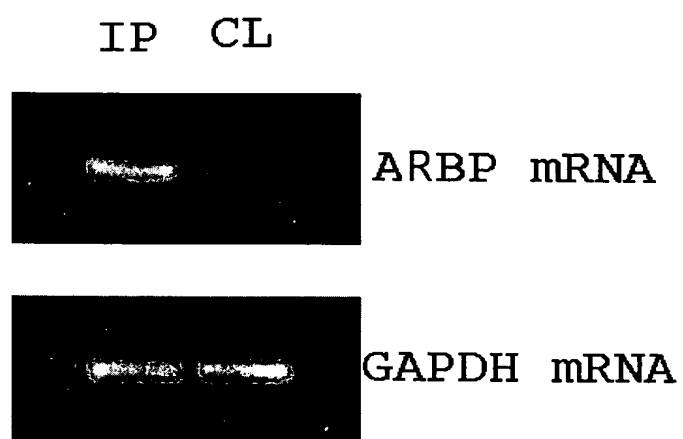


Figure 11

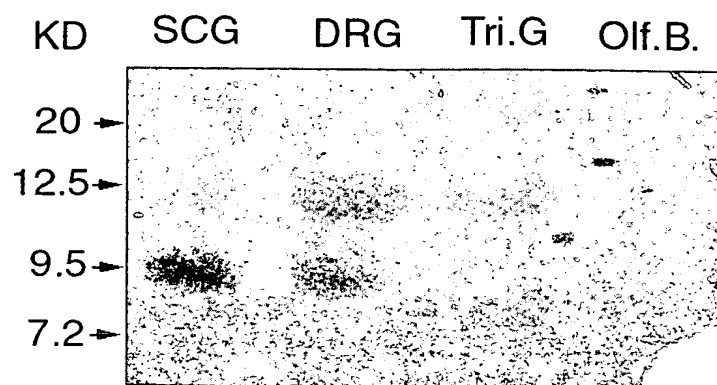


Figure 12

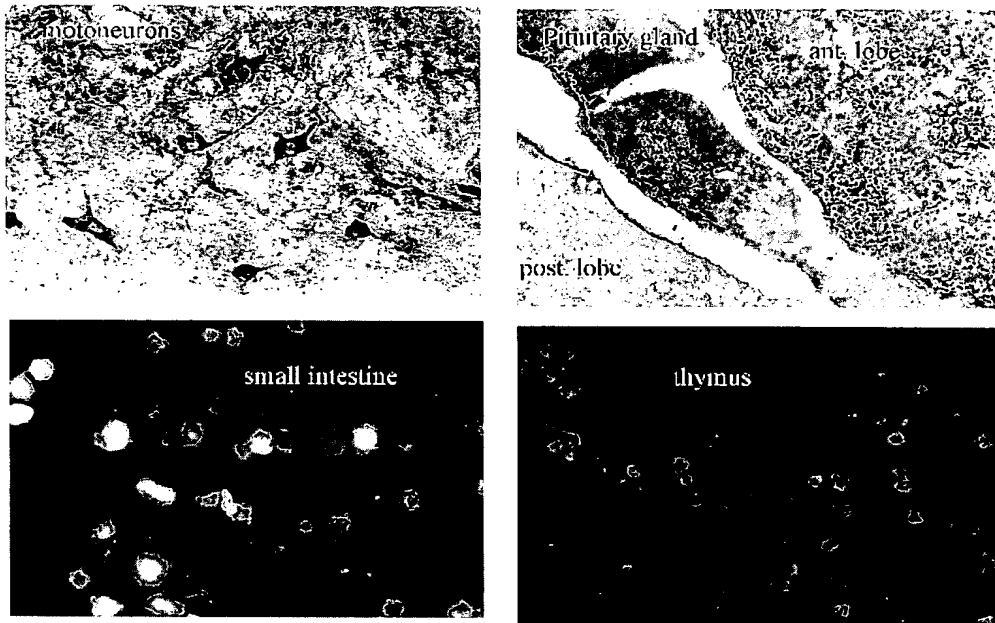


Figure 13

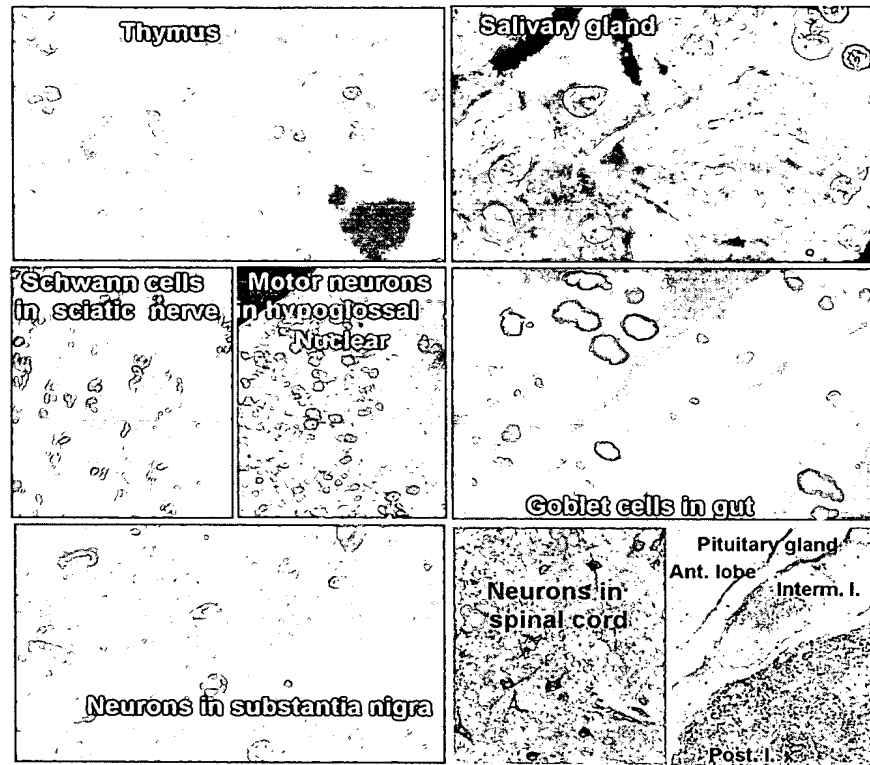
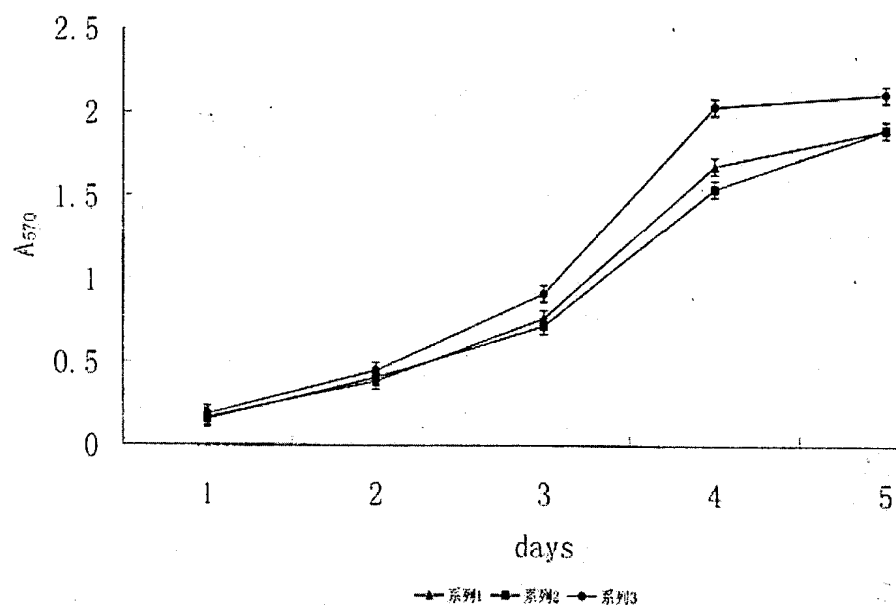


Figure 14



1, R2L1/R2L1-pcD 2, R2L1-ARBPF 3, R2L1-ARBPR

Figure 15

